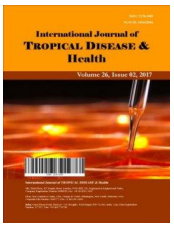

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Epidemiological Model for Pediatrics Patients with Leprosy Infection

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Authors' contributions

This work was carried out in collaboration among all authors. Author BBA designed the study, performed the statistical analysis, wrote the protocol and wrote the first draft of the manuscript. Authors AIV and AAO managed the analyses of the study. Author BBA managed the literature searches. All authors read and approved the final manuscript.

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ABSTRACT

Leprosy Infection (LI) is a long-term chronic infectious disease caused by the bacterium Mycobacterium leprae or Mycobacterium lepromatosis. This infectious disease has caused the public issue in many countries around the globe. The disease is prevalent among the adults, although there are now cases of the minor contacting this disease through household contact which is the primary source of infection such as (babysitters, neighbors). The emerging and reemerging diseases have led to a revived interest in infectious diseases in which mathematical models have become important tools in analyzing the spread and control of infectious diseases. Mathematical models are used in comparing, planning, implementing, evaluating and optimizing various detection, prevention therapy, and control programs, the model provides conceptual results such as threshold and basic reproduction number. In this paper, the Passive Immunity Pediatrics (M) - susceptible- Exposed-infected-recovered-susceptible (MSEIRS) model was adopted to depict the spread of infections in our environment.

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Keywords: Mathematical model; basic reproductive number; pediatrics patients; leprosy infection.

1. INTRODUCTION

The model uses the principles of epidemiological models, the idea is to investigate the particular details of an infection and express how individuals are progressing through a set of states at different rates. Leprosy is spread through a cough or contact with fluid from the nose of an infected person [1]. It occurs more commonly among those living in the rural area with extreme poverty, although, it is not highly contagious. Although, tuberculosis (TB) is not as prevalence as it was before now; the doctors do not take TB disease serious even when evaluating patients who have symptoms [2]. This resulted in the delay in diagnosis of TB disease in patients and the patient may sick and possibly infectious for a prolonged period [3]. There are two main types of leprosy disease which are based on the number of bacteria present: paucibacillary and multibacillary [4]. The two are differentiated by the number of poorly pigmented, numb skin patches present, with paucibacillary having five or fewer and multibacillary having more than five. Also, acid-fast bacilli can be used in the diagnosis biopsy of the skin or the use of polymerase chain reaction for detecting the DNA.

The greatest risk factor for been infected is been in contact with another case of leprosy, been in contacts with people living with leprosy are five to eight times more likely to develop leprosy than members of the general population. Other risk factors are conditions that reduce immune function, such malnutrition other illness, or host genetic differences which may increase the risk of developing leprosy [5]. These led to the need to development an effective and efficient epidemiological model that can be used to reduce the factors that are responsible for the prevalence of the disease in other to reduce leprosy infection. The epidemiological model which involves the individuals transition from a Passive Immunity to Susceptible state to Latent period to an Infectious one to a Recovered state at a certain rate, and become Susceptible again at a different rate. This model is called the MSEIRS model, because individuals move between them M (Passive Immunity in paediatrics), E (Latent period) S (Susceptible) and I (Infectious states) R (Recovered).

The Passive Immunity for pediatrics - Susceptible – Latent - Infected – Recovered-Susceptible (MSEIRS) model was introduced by Kermack and McKendrick, in 1927 [6]. In the model, the population is divided into three distinct groups of: the Passive Immunity for Infant (M), Latent period (E), Susceptible (S), Infected (I) and Recovered (R) where M, E, S, I and R represent the number of children in each of the groups respectively and the total population $N = M + E + S + I + R$. The Susceptibles are those who are not infected and not immune, the Infecteds are those who are infected and can transmit the disease, and the Recovered are those who are immune to re-infection. The characteristic feature of LI is that immunity after infection is temporary, such that the recovered can become susceptible again if all the risk factors are still present.

2. MATHEMATICAL MODEL FORMULATION

Passive immunity is an immunity obtained from external source: immunity from disease acquired by the transfer of antibodies from one person to another, e.g. through injections or between a mother and a fetus through the placenta looking at the case of infection spread on the population, there is an arrival of new susceptible population. In this type of situation, births and deaths rate must be included in the model. The differential equations represent the model which indicates the rate of change of number of individuals in each compartment with respect to time. Below is the Schematic diagram for the single age class M - Passive Immunity Infant, S- Susceptible, E – Latent period, I – Infectious, R – Recovered (MSEIRS) model for LI transmission (4).

An additional feature of LI is employed. By this Newborn babies whose mothers are immune are taken into consideration. As a result, these children are protected by the antibodies present in their mothers. Thus, group M of children who are completely protected by these antibodies are considered. The ratio of these newborn babies M is equal to the ratio of the general population that is immunized after recovering from infection. Protection reduces and these children M become susceptible at a rate. Under the above assumptions, the following are the results.

$$\frac{dM}{dt} = \mu - (+\mu)M, \qquad M(0) \tag{2.1}$$

$$\frac{dS}{dt} = M - \beta SI - \mu S + \gamma R, \quad S(0) \tag{2.2}$$

$$\frac{dE}{dt} = \beta SI - (\sigma + \mu)E, \quad E(0) \qquad 2.3$$

$$\frac{dI}{dt} = \sigma E - (v + \mu)I, \qquad I(0) \qquad 2.4$$

$$\frac{dR}{dt} = vI - (\mu + \gamma)R, \qquad R(0) \qquad 2.5$$

3. MODEL ANALYSIS

3.1 Two Classes of Epidemiology Models

Two different epidemiological models were formulated and analysed, they are Epidemic models and Endemic models. Epidemic model describe rapid outbreaks that occur in less than a year due to the availability of some risk factors, while endemic models are used for studying diseases of longer periods, during which there is a renewal of susceptible by births or recovery from temporary immunity.

The Virus – Free Equilibrium:

At equilibrium point

$$\frac{dM}{dt} = \frac{dS}{dt} = \frac{dE}{dt} = \frac{dI}{dt} = \frac{dR}{dt} = 0$$

Thus we have,

$$\frac{dM}{dt} = \mu - (+\mu)M = 0 \qquad 3.1$$

$$\frac{dS}{dt} = M - \beta SI - \mu S + \gamma R = 0 \qquad 3.2$$

$$\frac{dE}{dt} = \beta SI - (\sigma + \mu)E = 0 \qquad 3.3$$

$$\frac{dI}{dt} = \sigma E - (v + \mu)I = 0 \qquad 3.4$$

$$\frac{dR}{dt} = vI - (\mu + \gamma)R = 0 \qquad 3.5$$

From equations 3.1, 3.2, 3.3, 3.4 and 3.5 simultaneously, we obtained the Virus – free equilibrium

From equation 3.3

$$\sigma E - \mu I - vI = 0$$

Since the infection Free State is known to be diseases free, then,

I = 0, Thus

This become

$$\sigma E = 0, i.e\ E = 0$$

From equation 3.4

$$vI - \mu R - \gamma R = 0$$

Since, *I*=0, the equation becomes

$$-(\mu + \gamma)R = 0$$

Thus, R =0
Summary, *I*= 0, E =0 and R = 0
From equation 1.0

$$\mu - \varepsilon M - \mu M = 0$$
$$\mu = \varepsilon M + \mu M = 0$$
$$\mu = (\varepsilon + \mu)M$$

This gives

$$M = \frac{\mu}{\varepsilon + \mu}$$

From equation 3.1

Table 1. The description of parameters used in the model [7]

Parameter	Description	Unit
S	Susceptible population	Number/unit time
M	Birth rate of the children i.e the mortality rate	Number / unit time
I	Infected population	Number/unit time
R	Infected population that Recovered	Number/unit time
M	Passively immune infants	Number/unit time
$\boldsymbol{\mu}$	Birth rate of the children i.e the mortality rate	Number/unit time
γ	rate of loss of immunity	Number/unit time
ν	Rate of loss of infections	Number/unit time
ß	Transmission parameter (constant rate)	Number/unit time
R_0	Basic reproduction number	Number/unit time
Σ	Contact number	Number/unit time
E	Rate of loss of protection by maternal antibodies	Number/unit time

The unit time is (per year)

$\varepsilon M - \beta SI - \mu S + \gamma R = 0$

Since $I = 0$ and $R = 0$, this reduces to

$\varepsilon M - \mu S = 0$

$\varepsilon M = \mu S$

$MS = \frac{\varepsilon}{\mu}$

But

$$M = \frac{\mu}{\varepsilon + \mu}$$

Thus,

$$\frac{\varepsilon}{\mu} * \frac{\mu}{\varepsilon + \mu} = \frac{\varepsilon}{\varepsilon + \mu}$$

Finally for, virus free equilibrium, the solution set is as follows:

$$\left[M = \frac{\mu}{\varepsilon + \mu}, S = \frac{\varepsilon}{\varepsilon + \mu}, \quad E = 0, \quad I = 0, R = 0\right]$$

3.2 Establishing Local Stability for Virus-Free Equilibrium

We linearize the system of equations given, using the Jacobian matrix approach to obtain:

Evaluating the Jacobian matrix at the virus – free equilibrium E give

$$J(M,S,E,I,R)\begin{bmatrix} -\varepsilon-\mu & 0 & 0 & 0 & 0 \\ \varepsilon & -\beta I-\mu & 0 & -\beta S & \gamma \\ 0 & \beta I & -\mu-\sigma & \beta S & 0 \\ 0 & 0 & 0 & -\mu-\nu & 0 \\ 0 & 0 & 0 & \nu & -\mu-\gamma \end{bmatrix} = 0$$

We defined the characteristic polynomial equation for the J(E) solve for the eigen valves, to get: After a while, the eigenvalues λ_1, i=1,2,3,4,5 are given as

$\lambda_1 = -\mu$

$\lambda_2 = -\mu - \gamma$

$\lambda_3 = -\xi - \mu$

$\lambda_4 = \frac{1}{2(\xi+\mu)} [-2\mu^2 \mu\nu - 2\mu\varepsilon - \mu\sigma - \nu\varepsilon - \sigma\varepsilon + A]$

$\lambda_5 = \frac{-1}{2(\xi+\mu)} [2\mu^2 \mu\nu - 2\mu\varepsilon - \mu\sigma - \nu\varepsilon - \sigma\varepsilon + A]$

Where

$$A = \sqrt{\mu^2\nu^2 - 2\mu^2\nu\sigma + \mu^2\sigma^2 + 2\mu\nu^2\varepsilon - 2\mu\nu^2\varepsilon - 4\mu\nu\varepsilon\sigma + 4\mu\varepsilon\beta\sigma + 2\mu\varepsilon\sigma^2} + \nu^2\varepsilon^2 - 2\nu\varepsilon^2\sigma + 4\varepsilon^2\beta\sigma + \varepsilon^2\sigma^2$$

From the results above, $\lambda_1 < 0, \lambda_2 < 0$, $\lambda_3 < 0$,and $\lambda_5 < 0$ provided

$$\mu^2\nu^2 - 2\mu^2\nu\sigma + \mu^2\sigma^2 + 2\mu\nu^2\varepsilon - 4\mu\nu\varepsilon\sigma + 4\mu\varepsilon\beta\sigma + 2\mu\varepsilon\sigma^2 + \nu^2\varepsilon^2 - 2\nu\varepsilon^2\sigma + 4\varepsilon^2\beta\sigma + \varepsilon^2\sigma^2 \geq 0$$

That is,

$$\mu^2\nu^2 - \mu^2\sigma^2 + 2\mu\nu^2\varepsilon + 4\mu\varepsilon\beta\sigma + 2\mu\varepsilon\sigma^2 + \nu^2\varepsilon^2 + 4\varepsilon^2\varepsilon\sigma + \varepsilon^2\sigma^2 \geq 2\mu^2\nu\sigma + 4\mu\nu\varepsilon\sigma + 2\nu\varepsilon^2\sigma$$

So also, λ_4 must be less than zero, i.e, $\lambda_4 < 0$

hence,

$$\lambda_4 = \frac{1}{2(\varepsilon+\mu)} (-2\mu^2 - \mu\nu - 2\mu\varepsilon - \mu\sigma - \nu\varepsilon - \sigma\varepsilon + A) < 0,$$

which implies that ,

$$\frac{A}{2(\varepsilon+\mu)} < \frac{1}{2(\varepsilon+\mu)} (2\mu^2 - \mu\nu - 2\mu\varepsilon - \mu\sigma - \nu\varepsilon - \sigma\varepsilon)$$

That is

$$A < 2\mu^2 - \mu\nu - 2\mu\varepsilon - \mu\sigma - \nu\varepsilon - \sigma\varepsilon$$

Finally, the result is

$$R_0 = \frac{A}{2\mu^2 + \mu\nu + 2\mu\varepsilon + \mu\sigma + \nu\varepsilon + \sigma\varepsilon} < 1$$

A has been defined earlier above.

Where R_0 is the basic reproduction number, which is an important threshold in modelling of infectious diseases, since it tells us if a population is at risk from a disease or not. Thus, whenever R_0 < 1the new cases (i.e. incidence) of the disease will be on the decrease and the disease will eventually be eliminated.

Based on foregoing, the Basic Reproduction number (R_0) for our model is less than unity i.e

$$R_0 = \frac{A}{2\mu^2 + \mu\nu + 2\mu\varepsilon + \mu\sigma + \nu\varepsilon + \sigma\varepsilon} < 1$$

Then, I(t) decreases monotonically to zero as t → ∞. Therefore, the virus – free equilibrium is locally stable.

Local Stability for Virus – Endemic State:

$\frac{dM}{dt} = \frac{dS}{dt} = \frac{dE}{dt} = \frac{dI}{dt} = \frac{dR}{dt} = 0$

This gives

$$\frac{dM}{dt} = \mu - \varepsilon M - \mu M = 0 \qquad 3.6$$

$$\frac{dS}{dt} = \varepsilon M - \beta SI - \mu S + \gamma R = 0 \qquad 3.7$$

$$\frac{dE}{dt} = \beta SI - \sigma E - \mu E = 0 \qquad 3.8$$

$$\frac{dI}{dt} = \sigma E - \sigma E - \mu I - \nu I = 0 \qquad 3.9$$

$$\frac{dR}{dt} \nu I - \mu R - \gamma R = 0 \qquad 3.10$$

In this scenario, the state is assumed to be virus endemic, I >0

From equation 3.6

$$\mu - \varepsilon M - \mu M = 0$$
$$\mu = (\varepsilon + \mu)M = 0$$

$$M = \frac{\mu}{\varepsilon + \mu} \qquad 3.11$$

From equation 3.9

$$\sigma E - \mu I \nu I = 0$$

i.e ,

$$\sigma E = (\mu + \nu)I$$

Hence,

$$E = \frac{(\mu + \nu)}{\sigma} I \qquad 3.12$$

From equation 3.10

$$\nu I - \mu R - \gamma R = 0$$
$$\nu I = (\mu + \gamma)R$$
$$R = \left(\frac{\nu}{\mu + \gamma}\right) I \qquad 3.13$$

From equation 3.8

$$\beta SI - \sigma E - \mu E = 0$$
$$\beta SI = (\sigma \mu)E$$
$$S = \left(\frac{\sigma + \mu}{\beta I}\right) E$$

But $E = \left(\frac{\mu + \nu}{\sigma}\right) I$

Thus,

$$S = \left(\frac{\sigma + \mu}{\beta I}\right) E$$

$$S = \left(\frac{\sigma + \mu}{\beta I}\right)\left(\frac{\mu + \nu}{\sigma}\right) I$$

$$= \frac{(\delta + \mu)(\mu + \nu)}{\beta\sigma} \qquad 3.14$$

Substitute for M,E,R and S in Equation 3.7
$\varepsilon M - \beta SI - \mu S + \gamma R = 0$
That is:

$$\varepsilon * \frac{\mu}{\varepsilon + \mu} - \beta * \frac{(\delta + \mu)(\mu + \nu)}{\beta\sigma} * I - \mu * \frac{(\delta + \mu)(\mu + \nu)}{\beta\sigma} + \gamma^* \left(\frac{\nu}{\mu + \gamma}\right) I = 0$$

Solving for I yields:

$$I = \frac{-(\mu + \gamma)(\mu^3 + \mu^2\nu + \mu^2\varepsilon + \mu^2\sigma + \mu\nu\varepsilon + \mu\nu\sigma + \mu\varepsilon\sigma + \nu\varepsilon\sigma - \varepsilon\beta\sigma)}{\beta(\mu^3 + \mu^2\nu + \mu^2\varepsilon + \mu^2\gamma + \mu^2\sigma + \mu\nu\varepsilon + \mu\nu\gamma + \mu\nu\sigma + \mu\varepsilon\gamma + \mu\varepsilon\sigma + \mu\gamma\sigma + \nu\varepsilon\sigma + \varepsilon\gamma\sigma)}$$

Consequently,

$$R = (\frac{v}{\mu + \gamma})I$$

The above yields,

$$\frac{-v(\mu+\gamma)(\mu^3 + \mu^2 v + \mu^2\varepsilon + \mu^2\sigma + \mu v\sigma + \mu\varepsilon\sigma + v\varepsilon\sigma - \varepsilon\beta\sigma}{\beta(\mu^3 + \mu^2 v + \mu^2\varepsilon + \mu^2\gamma + \mu^2\sigma + \mu v\varepsilon + \mu v\gamma + \mu v\sigma + \mu\varepsilon\sigma + \mu\gamma\sigma + v\varepsilon\gamma + v\varepsilon\sigma + \varepsilon\gamma\sigma}$$

Also,

$$E = \left(\frac{\mu+v}{\sigma}\right) I$$
$$\frac{-v(\mu+\gamma)(\mu^3 + \mu^2 v + \mu^2\varepsilon + \mu^2\sigma + \mu v\sigma + \mu\varepsilon\sigma + v\varepsilon\sigma - \varepsilon\beta\sigma}{\beta\sigma(\mu^3 + \mu^2 v + \mu^2\varepsilon + \mu^2\gamma + \mu^2\sigma + \mu v\varepsilon + \mu v\gamma + \mu v\sigma + \mu\varepsilon\sigma + \mu\gamma\sigma + v\varepsilon\gamma + v\varepsilon\sigma + \varepsilon\gamma\sigma}$$

For mathematical acceptability, (M_E, S_E, E_E, I_E, R_E) > 0

Thus,

$$I_E = \frac{-v(\mu+\gamma)(\mu^3 + \mu^2 v + \mu^2\varepsilon + \mu^2\sigma + \mu v\sigma + \mu\varepsilon\sigma + v\varepsilon\sigma - \varepsilon\beta\sigma}{\beta(\mu^3 + \mu^2 v + \mu^2\varepsilon + \mu^2\gamma + \mu^2\sigma + \mu v\varepsilon + \mu v\gamma + \mu v\sigma + \mu\varepsilon\sigma + \mu\gamma\sigma + v\varepsilon\gamma + v\varepsilon\sigma + \varepsilon\gamma\sigma} > 0$$

Let,

$A = -(\mu + v)(\mu^3 + \mu^2 v + \mu^2\varepsilon + \mu^2\sigma + \mu v\varepsilon + \mu v\sigma + \mu\varepsilon\sigma + v\varepsilon\sigma)$
$B = \varepsilon\beta\sigma$ and,
$C = (\mu^3 + \mu^2 v + \mu^2\varepsilon + \mu^2\gamma + \mu^2\sigma + \mu v\varepsilon + \mu v\gamma + \mu v\sigma + \mu\varepsilon\sigma + \mu\gamma\sigma + v\varepsilon\gamma + v\varepsilon\sigma + \varepsilon\gamma\sigma))$

Hence,

$$I_E = \frac{(\mu + \gamma)(A - B)}{B * C} > 0$$
$$= -(\mu+\gamma)(A-B) > 0$$
$$= -(\mu+\gamma)A + B(\mu+\gamma) > 0$$
$$= B(\mu+\gamma) > (\mu+\gamma)A$$

Dividing through by A , we then have,

$$R_0 = \frac{B}{A} > 1$$

More elaborately, we have:

$$R_0 = \frac{\varepsilon\beta\sigma}{\mu^3 + \mu^2 v + \mu^2\varepsilon + \mu^2\sigma + \mu v\varepsilon + \mu v\sigma + \mu\varepsilon\sigma + v\varepsilon\sigma} > 1$$

If β 64.5, *v* = 36, ε= 13, δ= 91, μ =0.041 are all parameter for a period of one year, then we have the following expression:

$$\frac{13 * 64.5 * 91}{(0.041)^3 + (0.041)^2 36 + (0.041)^2 13 + (0.041)^2 91 + (0.041)(36)(13) + (0.041)(36)(91) + (0.041)(91)(13) + (36)(13)(91)} > 1$$

$$R_0 = 2.944076535 > 1$$

If R_0 > 1 then I (t) increases and reaches its maximum and reduces as $R_0 \to \infty$. When the number of children infected increases in this state, it is called the epidemic state. In the long run, the whole population become susceptible if R_0 > 1.

4. NUMERICAL SOLUTION AND SIMULATION

The MSEIRS model was solved numerically using Runge – Kutta method, Matlab ode45 program was adopted, which is based on an explicit Runge Kutta (4, 5) formula. Runge kutta of order four is also used in plotting the graphs; it's a powerful and popular method because of its accuracy and stability. Also, its simplicity and stability make it one of the most widely used numerical algorithms for stiff and non-stiff equations, it converges faster than that of order two or three.

These are the parameters used in plotting the graphs: although some of it changes, since they are the major factors that determining the situations of the environment, whether it is of the virus –free and endemic state.

The graph of MSEIRS model is used to monitor our environment in case of an outbreak of leprosy based dynamics of the number of on changes on a particular model parameter.

Fig. 1 shows the graphical representation of MSEIRS model between the space of one year. In these model, newborn infants of immune mothers that are protected by maternal antibodies, but later got infected through babysitter or through the infected neighbours. They recovered after been treated but since, they domicile in the same infected area, the protected infants become susceptible again.

Table 2. Simulating the MSEIRS model using the following parameter values

Parameters	*V*	b_0	b_1	δ	Φ	μ	γ	ζ	β	R_0
MSEIRS (Virus free State	36	50	0.14	91	0.15	0.041	1.8	13	64.5	0.9515728172
MSEIRS (Epidemic State)	36	20	0.20	91	0.15	0.041	1.8	13	27	2.944076535

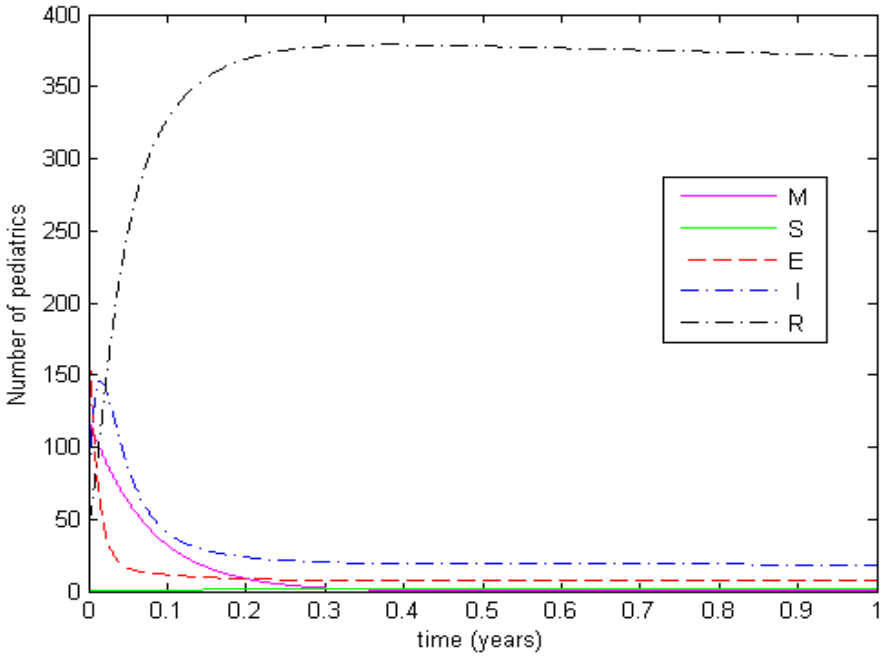

Fig. 1. Graphical representation of MSEIRS model between the space of one year with M_0 = 120, S_0 = 100 ,E_0 = 82 , I_0 =67, R_0 = 46 [7]

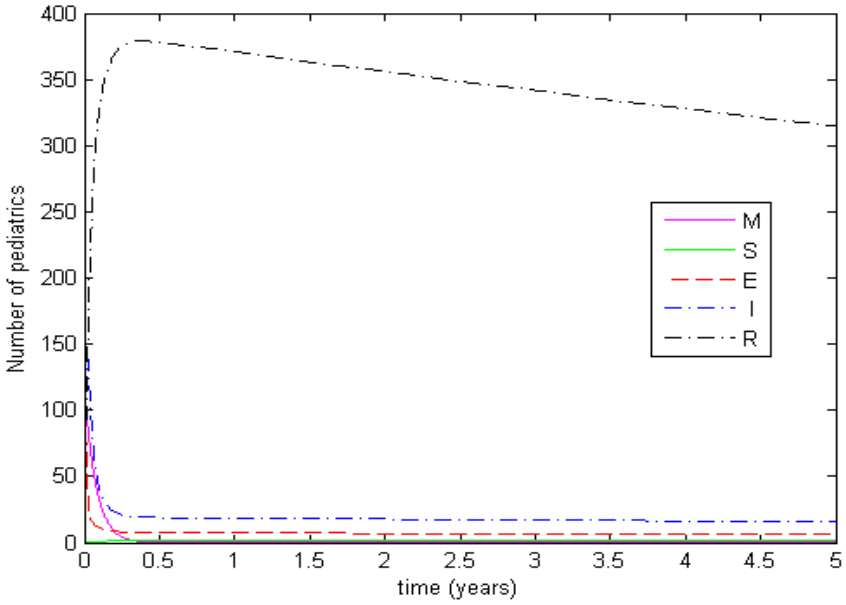

Fig. 2. Graphical respresentation of MSEIRS model between the space of five years [7]

Fig. 2 shows the graphical representation of MSEIRS model between the space of five years. In these model, These set of children were assumed to be of primary school age, they have the oppourtunity of playing around with their school mates. Some are born are born completely protected while some are from the infected parents. The protected onces are infected but recovered through vacination but since they were in the same enviroment they become susceptible again.

5. CONCLUSION

The MSEIRS model is used as a benchmark for modeling infectious disease, since the existence of a threshold for infection is far from obvious. The model mathematical analysis was calculated to know if the model is mathematically feasible, also, the local stability was calculated to know if our enviroment is of virus – free or of an endemic equilibrium. The threshold value was set through the calculation of the basic reproductive number R_0 which is an important part of modelling disease to tell us if the population is at risk or not.

CONSENT

It is not applicable.

ETHICAL APPROVAL

It is not applicable.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

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